OIPE 0400
03/09/01

INPUT SET: S36561.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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1                                   SEQUENCE LISTING      ENTERED
2
3      (1)      General Information:
4
5           (i) APPLICANT: Reed, John C.
6                          Sato, Takaaki
7
8          (ii) TITLE OF INVENTION: CD40 Associated Proteins
9
10       (iii) NUMBER OF SEQUENCES: 17
11
12        (iv) CORRESPONDENCE ADDRESS:
13               (A) ADDRESSEE: Campbell and Flores
14               (B) STREET: 4370 La Jolla Village Drive, Suite 700
15               (C) CITY: San Diego
16               (D) STATE: California
17               (E) COUNTRY: USA
18               (F) ZIP: 92122
19
20         (v) COMPUTER READABLE FORM:
21               (A) MEDIUM TYPE: Floppy disk
22               (B) COMPUTER: IBM PC compatible
23               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24               (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26        (vi) CURRENT APPLICATION DATA:
27               (A) APPLICATION NUMBER:09/757,041
28               (B) FILING DATE:
29               (C) CLASSIFICATION:
30
31       (vii) PRIOR APPLICATION DATA:
32               (A) APPLICATION NUMBER:08/349,357
33               (B) FILING DATE:
34
35
36
37      (viii) ATTORNEY/AGENT INFORMATION:
38               (A) NAME: Campbell, Cathryn A.
39               (B) REGISTRATION NUMBER: 31,815
40               (C) REFERENCE/DOCKET NUMBER: P-LJ 1203
41
42        (ix) TELECOMMUNICATION INFORMATION:
43               (A) TELEPHONE: (619) 535-9001
44               (B) TELEFAX: (619) 535-8949
45
46
```

INPUT SET: S36561.raw

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47    (2) INFORMATION FOR SEQ ID NO:1:
48
49         (i) SEQUENCE CHARACTERISTICS:
50              (A) LENGTH: 2240 base pairs
51              (B) TYPE: nucleic acid
52              (C) STRANDEDNESS: single
53              (D) TOPOLOGY: linear
54
55
56        (ix) FEATURE:
57              (A) NAME/KEY: CDS
58              (B) LOCATION: 137..1766
59
60
61        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63    AGAAGTGATG CCACTTGGTT AAGGTCCCAG AGCAGGTCAG AATCAGACCT AGGATCAGAA      60
64
65    ACCTGGCTCC TGGCTCCTGG CTCCCTACTC TTCTAAGGAT CGCTGTCCTG ACAGAAGAGA     120
66
67    ACTCCTCTTT CCTAAA ATG GAG TCG AGT AAA AAG ATG GAC TCT CCT GGC         169
68                     Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly
69                      1               5                  10
70
71    GCG CTG CAG ACT AAC CCG CCG CTA AAG CTG CAC ACT GAC CGC AGT GCT      217
72    Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala
73            15                  20                  25
74
75    GGG ACG CCA GTT TTT GTC CCT GAA CAA GGA GGT TAC AAG GAA AAG TTT      265
76    Gly Thr Pro Val Phe Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe
77            30                  35                  40
78
79    GTG AAG ACC GTG GAG GAC AAG TAC AAG TGT GAG AAG TGC CAC CTG GTG      313
80    Val Lys Thr Val Glu Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val
81        45                  50                  55
82
83    CTG TGC AGC CCG AAG CAG ACC GAG TGT GGG CAC CGC TCC TGC GAG AGC      361
84    Leu Cys Ser Pro Lys Gln Thr Glu Cys Gly His Arg Ser Cys Glu Ser
85    60                  65                  70                  75
86
87    TGC ATG GCG GCC CTG CTG AGC TCT TCA AGT CCA AAA TGT ACA GCG TGT      409
88    Cys Met Ala Ala Leu Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys
89                    80                  85                  90
90
91    CAA GAG AGC ATC GTT AAA GAT AAG GTG TTT AAG GAT AAT TGC TGC AAG      457
92    Gln Glu Ser Ile Val Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys
93                    95                 100                 105
94
95    AGA GAA ATT CTG GCT CTT CAG ATC TAT TGT CGG AAT GAA AGC AGA GGT      505
96    Arg Glu Ile Leu Ala Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly
97            110                 115                 120
98
99    TGT GCA GAG CAG TTA ACG CTG GGA CAT CTG CTG GTG CAT TTA AAA AAT      553
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100    Cys Ala Glu Gln Leu Thr Leu Gly His Leu Leu Val His Leu Lys Asn
101        125             130             135
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103    GAT TGC CAT TTT GAA GAA CTT CCA TGT GTG CGT CCT GAC TGC AAA GAA      601
104    Asp Cys His Phe Glu Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu
105    140             145             150             155
106
107    AAG GTC TTG AGG AAA GAC CTG CGA GAC CAC GTG GAG AAG GCG TGT AAA      649
108    Lys Val Leu Arg Lys Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys
109                    160             165                 170
110
111    TAC CGG GAA GCC ACA TGC AGC CAC TGC AAG AGT CAG GTT CCG ATG ATC      697
112    Tyr Arg Glu Ala Thr Cys Ser His Cys Lys Ser Gln Val Pro Met Ile
113                175             180             185
114
115    GCG CTG CAG AAA CAC GAA GAC ACC GAC TGT CCC TGC GTG GTG GTG TCC      745
116    Ala Leu Gln Lys His Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser
117            190             195             200
118
119    TGC CCT CAC AAG TGC AGC GTC CAG ACT CTC CTG AGG AGC GAG GGG ACA      793
120    Cys Pro His Lys Cys Ser Val Gln Thr Leu Leu Arg Ser Glu Gly Thr
121        205             210             215
122
123    AAC CAG CAG ATC AAG GCC CAC GAG GCC AGC TCC GCC GTG CAG CAC GTC      841
124    Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val Gln His Val
125    220             225             230             235
126
127    AAC CTG CTG AAG GAG TGG AGC AAC TCG CTC GAA AAG AAG GTT TCC TTG      889
128    Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu
129                    240             245             250
130
131    TTG CAG AAT GAA AGT GTA GAA AAA AAC AAG AGC ATA CAA AGT TTG CAC      937
132    Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His
133                255             260             265
134
135    AAT CAG ATA TGT AGC TTT GAA ATT GAA ATT GAG AGA CAA AAG GAA ATG      985
136    Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met
137            270             275             280
138
139    CTT CGA AAT AAT GAA TCC AAA ATC CTT CAT TTA CAG CGA GTG ATA GAC      1033
140    Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp
141        285             290             295
142
143    AGC CAA GCA GAG AAA CTG AAG GAG CTT GAC AAG GAG ATC CGG TCC TTC      1081
144    Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile Arg Ser Phe
145    300             305             310             315
146
147    CGG CAG AAC TGG GAG GAA GCA GAC AGC ATG AAG AGC AGC GTG GAG TCC      1129
148    Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser
149                    320             325             330
150
151    CTC CAG AAC CGC GTG ACC GAG CTG GAG AGC GTG GAC AAG AGC GCG GGG      1177
152    Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/757,041

INPUT SET: S36561.raw

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155   CAA GTG GCT CGG AAC ACA GGC CTG CTG GAG TCC CAG CTG AGC CGG CAT      1225
156   Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His
157           350                    355                    360
158
159   GAC CAG ATG CTG AGT GTG CAC GAC ATC CGC CTA GCC GAC ATG GAC CTG      1273
160   Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp Met Asp Leu
161           365                    370                    375
162
163   CGC TTC CAG GTC CTG GAG ACC GCC AGC TAC AAT GGA GTG CTC ATC TGG      1321
164   Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp
165   380                    385                    390                    395
166
167   AAG ATT CGC GAC TAC AAG CGG CGG AAG CAG GAG GCC GTC ATG GGG AAG      1369
168   Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys
169                    400                    405                    410
170
171   ACC CTG TCC CTT TAC AGC CAG CCT TTC TAC ACT GGT TAC TTT GGC TAT      1417
172   Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr
173           415                    420                    425
174
175   AAG ATG TGT GCC AGG GTC TAC CTG AAC GGG GAC GGG ATG GGG AAG GGG      1465
176   Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly
177           430                    435                    440
178
179   ACG CAC TTG TCG CTG TTT TTT GTC ATC ATG CGT GGA GAA TAT GAT GCC      1513
180   Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala
181           445                    450                    455
182
183   CTG CTT CCT TGG CCG TTT AAG CAG AAA GTG ACA CTC ATG CTG ATG GAT      1561
184   Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp
185   460                    465                    470                    475
186
187   CAG GGG TCC TCT CGA CGT CAT TTG GGA GAT GCA TTC AAG CCC GAC CCC      1609
188   Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro
189                    480                    485                    490
190
191   AAC AGC AGC AGC TTC AAG AAG CCC ACT GGA GAG ATG AAT ATC GCC TCT      1657
192   Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser
193           495                    500                    505
194
195   GGC TGC CCA GTC TTT GTG GCC CAA ACT GTT CTA GAA AAT GGG ACA TAT      1705
196   Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr
197           510                    515                    520
198
199   ATT AAA GAT GAT ACA ATT TTT ATT AAA GTC ATA GTG GAT ACT TCG GAT      1753
200   Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp
201           525                    530                    535
202
203   CTG CCC GAT CCC T GATAAGTAGC TGGGGAGGTG GATTTAGCAG AAGGCAACTC         1806
204   Leu Pro Asp Pro
205   540
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INPUT SET: S36561.raw

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206
207   CTCTGGGGGA TTTGAACCGG TCTGTCTTCA CTGAGGTCCT CGCGCTCAGA AAAGGACCTT   1866
208
209   GTGAGACGGA GGAAGCGGCA GAAGGCGGAC GCGTGCCGGC GGGAGGAGCC ACGCGTGAGA   1926
210
211   CACCTGACAC GTTTTATAAT AGACTAGCCA CACTTCACTC TGAAGAATTA TTTATCCTTC   1986
212
213   AACAAGCATA AATATTGCTG TCAGAGAAGG TTTTCATTTT CATTTTTAAA GATCTAGTTA   2046
214
215   ATTAAGGTGG AAAACATATA TGCTAAACAA AAGAAACATG ATTTTTCTTC CTTAAACTTG   2106
216
217   AACACCAAAA AACACACACA CACACACACA CGTGGGGATA GCTGGACATG TCAGCATGTT   2166
218
219   AAGTAAAAGG AGAATTTATG AAATAGTAAT GCAATTCTGA TATCTTCTTT CTAAAATTCA   2226
220
221   AGAGTGCAAT TTTG                                                       2240
222
223
224   (2) INFORMATION FOR SEQ ID NO:2:
225
226           (i) SEQUENCE CHARACTERISTICS:
227                 (A) LENGTH: 543 amino acids
228                 (B) TYPE: amino acid
229                 (D) TOPOLOGY: linear
230
231           (ii) MOLECULE TYPE: protein
232
233           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
234
235   Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
236    1               5                  10                  15
237
238   Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
239                20                  25                  30
240
241   Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
242                35                  40                  45
243
244   Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
245             50                  55                  60
246
247   Gln Thr Glu Cys Gly His Arg Ser Cys Glu Ser Cys Met Ala Ala Leu
248    65                  70                  75                  80
249
250   Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
251                      85                  90                  95
252
253   Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
254                100                 105                 110
255
256   Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
257             115                 120                 125
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/757,041*

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